

JUL 05 2001

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/297,486

DATE: 06/12/2001

TIME: 13:11:24

Input Set : A:\GJE-30.txt

Output Set: N:\CRF3\06122001\I297486.raw

ENTERED

4,2
7-9-01
P.Z.

4 <110> APPLICANT: Martin, John Francis
 5 Yla-Herttuala, Seppo
 6 Barker, Stephen George Edward
 8 <120> TITLE OF INVENTION: Therapeutic Use of an Agent That Stimulates NO or
 Prostacyclin Production
 9 and Delivery Device
 11 <130> FILE REFERENCE: GJE-30
 13 <140> CURRENT APPLICATION NUMBER: US 09/297,486
 C--> 14 <141> CURRENT FILING DATE: 2001-05-24
 16 <150> PRIOR APPLICATION NUMBER: PCT/GB97/03015
 17 <151> PRIOR FILING DATE: 1997-11-03
 19 <150> PRIOR APPLICATION NUMBER: GB 9622852.3
 20 <151> PRIOR FILING DATE: 1996-11-01
 22 <150> PRIOR APPLICATION NUMBER: GB 9709494.0
 23 <151> PRIOR FILING DATE: 1997-05-09
 25 <150> PRIOR APPLICATION NUMBER: GB 9717791.9
 26 <151> PRIOR FILING DATE: 1997-08-21
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 32 <211> LENGTH: 441
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens
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 37 <221> NAME/KEY: CDS
 38 <222> LOCATION: 1..441
 40 <400> SEQUENCE: 1
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 43 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 44 1 5 10 15
 46 tac ctc cac cat gcc aag tgg tcc cag gct gca ccc atg gca gaa gga 96
 47 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 48 20 25 30
 50 gga ggg cag aat cat cac gaa gtg gtg aag ttc atg gat gtc tat cag 144
 51 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 52 35 40 45
 54 cgc agc tac tgc cat cca atc gag acc ctg gtg gac atc ttc cag gag 192
 55 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 56 50 55 60
 58 tac cct gat gag atc gag tac atc ttc aag cca tcc tgt gtg ccg ctg 240
 59 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 60 65 70 75 80
 62 atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg gag tgt gtg ccc 288
 63 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 64 85 90 95
 66 act gag gag tcc aac atc acc atg cag att atg cgg atc aaa cct cac 336
 67 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 68 100 105 110
 70 caa ggc cag cac ata gga gag atg agc ttc cta cag cac aac aaa tgt 384

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71 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
72      115      120      125
74 gaa tgc aga cca aag aaa gat aga gca aga caa gaa aaa tgt gac aag      432
75 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
76      130      135      140
78 ccg agg cgg      441
79 Pro Arg Arg
80 145
83 <210> SEQ ID NO: 2
84 <211> LENGTH: 147
85 <212> TYPE: PRT
86 <213> ORGANISM: Homo sapiens
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91      1      5      10      15
93 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
94      20      25      30
96 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
97      35      40      45
99 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
100      50      55      60
102 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
103      65      70      75      80
105 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
106      85      90      95
108 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
109      100      105      110
111 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
112      115      120      125
114 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
115      130      135      140
117 Pro Arg Arg
118 145
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 573
123 <212> TYPE: DNA
124 <213> ORGANISM: Homo sapiens
126 <220> FEATURE:
127 <221> NAME/KEY: CDS
128 <222> LOCATION: 1..573
130 <400> SEQUENCE: 3
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134      1      5      10      15
136 tac ctc cac cat gcc aag tgg tcc cag gct gca ccc atg gca gaa gga      96
137 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
138      20      25      30
140 gga ggg cag aat cat cac gaa gtg gtg aag ttc atg gat gtc tat cag      144
141 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln

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142          35          40          45
144 cgc agc tac tgc cat cca atc gag acc ctg gtg gac atc ttc cag gag      192
145 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
146          50          55          60
148 tac cct gat gag atc gag tac atc ttc aag cca tcc tgt gtg ccg ctg      240
149 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
150 65          70          75          80
152 atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg gag tgt gtg ccc      288
153 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
154          85          90          95
156 act gag gag tcc aac atc acc atg cag att atg cgg atc aaa cct cac      336
157 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
158          100          105          110
160 caa ggc cag cac ata gga gag atg agc ttc cta cag cac aac aaa tgt      384
161 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
162          115          120          125
164 gaa tgc aga cca aag aaa gat aga gca aga caa gaa aaa ccc tgt ggg      432
165 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Pro Cys Gly
166          130          135          140
168 cct tgc tca gag cgg aga aag cat ttg ttt gta caa gat ccg cag acg      480
169 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
170 145          150          155          160
172 tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc aag gcg agg cag      528
173 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
174          165          170          175
176 ctt gag tta aac gaa cgt act tgc aga tgt gac aag ccg agg cgg      573
177 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
178          180          185          190
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 191
183 <212> TYPE: PRT
184 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 4
188 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
189 1          5          10          15
191 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
192          20          25          30
194 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
195          35          40          45
197 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
198          50          55          60
200 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
201 65          70          75          80
203 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
204          85          90          95
206 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
207          100          105          110
209 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
210          115          120          125

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212 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Pro Cys Gly
213      130      135      140
215 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
216 145      150      155      160
218 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
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221 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
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225 <211> LENGTH: 645
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229 <220> FEATURE:
230 <221> NAME/KEY: CDS
231 <222> LOCATION: 1..645
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236 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
237 1      5      10      15
239 tac ctc cac cat gcc aag tgg tcc cag gct gca ccc atg gca gaa gga      96
240 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
241      20      25      30
243 gga ggg cag aat cat cac gaa gtg gtg aag ttc atg gat gtc tat cag      144
244 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
245      35      40      45
247 cgc agc tac tgc cat cca atc gag acc ctg gtg gac atc ttc cag gag      192
248 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
249      50      55      60
251 tac cct gat gag atc gag tac atc ttc aag cca tcc tgt gtg ccg ctg      240
252 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
253 65      70      75      80
255 atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg gag tgt gtg ccc      288
256 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
257      85      90      95
259 act gag gag tcc aac atc acc atg cag att atg cgg atc aaa cct cac      336
260 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
261      100      105      110
263 caa ggc cag cac ata gga gag atg agc ttc cta cag cac aac aaa tgt      384
264 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
265      115      120      125
267 gaa tgc aga cca aag aaa gat aga gca aga caa gaa aaa aaa tca gtt      432
268 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val
269      130      135      140
271 cga gga aag gga aag ggg caa aaa cga aag cgc aag aaa tcc cgg tat      480
272 Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr
273 145      150      155      160
275 aag tcc tgg agc gtg ccc tgt ggg cct tgc tca gag cgg aga aag cat      528
276 Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His
277      165      170      175

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```

280 ttg ttt gta caa gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca      576
281 Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr
282              180              185              190
284 gac tcg cgt tgc aag gcg agg cag ctt gag tta aac gaa cgt act tgc      624
285 Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys
286              195              200              205
288 aga tgt gac aag ccg agg cgg      645
289 Arg Cys Asp Lys Pro Arg Arg
290      210              215
293 <210> SEQ ID NO: 6
294 <211> LENGTH: 215
295 <212> TYPE: PRT
296 <213> ORGANISM: Homo sapiens
298 <400> SEQUENCE: 6
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301      1              5              10              15
303 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
304              20              25              30
306 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
307              35              40              45
309 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
310              50              55              60
312 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
313      65              70              75              80
315 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
316              85              90              95
318 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
319              100              105              110
321 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
322              115              120              125
324 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val
325              130              135              140
327 Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr
328      145              150              155              160
330 Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His
331              165              170              175
333 Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr
334              180              185              190
336 Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys
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340      210              215
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344 <211> LENGTH: 696
345 <212> TYPE: DNA
346 <213> ORGANISM: Homo sapiens
348 <220> FEATURE:
349 <221> NAME/KEY: CDS
350 <222> LOCATION: 1..696

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VERIFICATION SUMMARY

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Input Set : A:\GJE-30.txt

Output Set: N:\CRF3\06122001\I297486.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date